

SUPPORT FOR THE AMENDMENTS

Claims 2, 3, 9, and 10 were previously canceled.

Claims 1 and 7 have been amended.

The amendment of Claims 1 and 7 is supported by original Claims 1 and 5-7.

No new matter has been added by the present amendments.

REMARKS

Claims 1, 4-8, and 11-16 are pending in the present application.

The rejections of Claims 1, 4-8, and 11-16 under 35 U.S.C. §112, first paragraph (enablement), is respectfully traversed.

The Examiner appears to recognize that the specification is enabling for a mutant plant in the family Brassicaceae, obtained by chemical mutagenesis, and comprising a mutant gene encoding a protein comprising the amino acid sequence SEQ ID NO: 7. However, the Examiner alleges that the specification fails to enable an isolated mutant gene encoding a protein comprising the amino acid sequence GYX₁VEX₂, wherein X₁ is R or N and X₂ is a basic amino acid, or for transgenic plants transformed with said gene.

Applicants respectfully disagree with the Examiner's allegations with respect to a purported lack of enablement. To this end, Applicants submit that the information provided by the specification combined with the prior art knowledge is sufficient to allow one of skill in the art to produce and isolate the mutant sequence.

In the specification, it is disclosed that the mutant gene is derived from a sequence encoding a protein of the RGA/GAI subgroup of the GRAS family, that the wild-type protein must comprise the sequence GYRVEE or GYNVEE, and that the claimed mutation results in the substitution of the C-terminal "E" of this sequence with R or K. The specification further provides the full-length sequences of wild-type and mutant cDNAs and proteins.

At the time of the present invention, the GRAS family and the RGA/GAI subfamily (DELLA family) were known in the art (see, for example, page 8 of the response filed on November 8, 2006), and conserved sequence motifs allowing the recognition of whether a protein belongs to the GRAS family, and more specifically to the RGA/GAI subfamily were

clearly defined. To support this position, the Examiner's attention is directed to the publications of Peng et al. (1999) (cited by the Examiner in the Office Action mailed July 29, 2005), and the publication of Silverstone et al. (1998) (Annex 1 to the response filed on November 8, 2006). Thus, it would have been only a matter of routine experimentation to query the sequence databases with the full-length sequences disclosed in the present specification, to identify those corresponding to proteins of the RGA/GAI subfamily having a GYRVEE or GYNVEE sequence, and to isolate the corresponding gene.

Alternatively, one of skill in the art would also have been able to design, from the highly conserved sequences within the RGA/GAI subfamily and from the sequence information provided by the present specification, appropriate probes and/or primers allowing isolation of a cDNA encoding a protein belonging to the RGA/GAI subfamily and comprising the sequence GYRVEE or GYNVEE from a cDNA library of a plant without undue experimentation. Once the wild-type cDNA is isolated, it is also only a matter of routine experimentation to perform directed mutagenesis in order to replace the codon for "E" with a codon for "R" or "K".

Further, once the mutant sequence is obtained, inserting it in an appropriate construct and performing plant transformation is also well within the ordinary skill in the art. The Examiner's comments referring to the unpredictable results which are obtained when transforming plants with genes that are involved in plant development are not relevant, since they refer to a state of the art concerning genes that do not encode proteins of the RGA/GAI family, and that are not even related to the GRAS family. REB is a basic leucine-zipper (bZIP) transcription factor, OSH1 is an homeobox transcription factor, and CBFs belong to the AP2/EREBP family.

The present invention concerns a mutant transcription factor of the RGA/GAI family. Thus, the prior art to be considered should relate to transgenic plants expressing mutant transcription factors of the RGA/GAI family. Peng et al. (1999) disclose several mutants of RGA/GAI transcription factors. Although they do not involve the same part of the protein, all the mutations disclosed by Peng et al. are functionally similar to the mutation disclosed in the present application, i.e. they are semi-dominant mutations that confer a dwarf, gibberellin-resistant phenotype. Peng et al. further disclose (see page 261 "Rice transformants", and Figure 4) the production of transgenic rice expressing a mutant gene of Arabidopsis, under control of the ubiquitin maize promoter (which is a well-known constitutive and ubiquitous promoter). All the plants containing the transgene have a dwarf gibberellin-resistant phenotype.

It clearly appears from the prior art that transformation of plants by a gene encoding a mutant results in transgenic plants having the desired phenotype, without having to choose a promoter providing a specific pattern of expression, and without performing screening steps other than the classical detection of the transgene. Thus, there is no reason to presume that replacing the RGA/GAI mutant gene of Peng et al. by the RGA/GAI mutant gene of the invention will not allow producing, in the same way, transgenic plants having the desired phenotype.

Therefore, in view of the information provided by the specification combined with the prior art knowledge one of skill in the art would have been able to practice the claimed invention without undue experimentation.

In view of the foregoing, Applicants request withdrawal of these grounds of rejection.

The rejection of Claims 5-8, 11, and 13-16 under 35 U.S.C. §102(b) over Foisset et al taken with the evidence of Barret et al is respectfully traversed.

The Examiner states again that Foisset et al anticipate the present invention because this publication is cited in the specification as reporting the existence of a plant having the *bzh* gene that is responsible for the mutant phenotype. However, the Examiner has not explained how Foisset et al provide an enabling disclosure of this mutant plant, *i.e.* a disclosure that combined with knowledge in the prior art, would allow one of ordinary skill in the art to grow and cultivate the plant (MPEP 2121.03).

Actually, Foisset et al disclose that the mutation results from with EMS. Following this teaching, one of skill in the art is able to perform chemical mutagenesis of seeds, to grow all the plants from the mutagenized seeds and to select the plants that have a reduced development. He is likely to obtain many plants having a reduced development, since, as already explained in the response to the previous Office Actions, many genes have been identified as involved in dwarfism (and probably, many genes not yet identified are also involved). The Examiner is reminded that EMS mutagenesis is non-discriminatory. EMS mutagenesis primarily induces G→A substitutions. Therefore, the only suggestion that the skilled artisan would take from Foisset et al is that the *bzh* mutation is likely a G→A substitution. However, the size of the rapeseed genome is about 1200×10^6 bp. If one considers a G/C content of approximately 50%, there would be about 600×10^6 possible G→A substitutions genome-wide. Clearly, the disclosure of Foisset et al is would not place the skilled artisan in of the specific *bzh* mutant plant of the present invention, much less provide information on the gene involved in the *bzh* mutation or the position of the mutation within this gene. Put simply, the skilled artisan would have no means to determine whether

or not one of the plants selected after EMS mutagenesis has the same *bzh* mutation as in the presently claimed invention.

Barret et al further disclose that the *bzh* mutation is semi-dominant. In order to determine if one or more of the EMS mutants selected on the basis of their reduced development has a semi-dominant mutation, the skilled artisan would have to study the progeny of each of these mutants by performing appropriate crosses to obtain homozygous and heterozygous plants for each of the mutation in order to compare them. If the mutation is semi-dominant the homozygous plants should be dwarf, while the heterozygous plants should be semi-dwarf. This will involve clearly a great amount of experimentation, in particular in view of the fact that it may be difficult to distinguish the homozygous dwarf plants from the heterozygous semi-dwarf ones, due to the influence of both the genetic background and the environment on the expression of this character, as indicated by Barret et al (page 828, 2nd column 1st paragraph).

Further, even if one succeeds at identifying plants having a semi-dominant mutation, he will still not be able to determine whether or not there is among them a plant with the *bzh* mutation, since he will have no means to detect this particular mutation and thus to differentiate it from other mutants having a similar phenotype. Thus, he will not be in possession of the *bzh* mutant plant reported by Foisset et al.

Accordingly, withdrawal of this ground of rejection is requested.

Finally, the Examiner's objection to Claim 7 under 37 C.F.R. §1.75(c) as failing to further limit Claim 6 from which it depends is obviated by amendment. Applicants have changed the dependency of Claim 7 to depend from Claim 5. Thus, this ground of criticism is moot. Acknowledgement that this ground of objection has been withdrawn is requested.

Applicants submit that the present application is in condition for allowance. Early notification to this effect is respectfully requested.

Respectfully submitted,

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